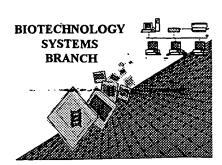


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

and the second

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY ----or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2Kcompliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u> http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Erro Summary

ERROR DETECTED SUGGESTED CORRECTION

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	ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/636530
ATTN:	NEW RULES CASES: PI	LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
AT	Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line.
	mapped macicles	This may occur if your file was retrieved in a word processor after creating it.
		Please adjust your right margin to .3, as this will prevent "wrapping".
		ricase adjust your ngin margin to .o, as this will prevent wropping .
)	Wrapped Aminos	The amino acid number/text at the end of each line "wrapped " down to the next line.
	wapped Aminos	This may occur if your file was retrieved in a word processor after creating it.
		•
		Please adjust your right margin to .3, as this will prevent "wrapping".
	Incorrect Line Longth	The subscreening that a line pat exceed 72 characters in length. This includes snaces
-T	Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
		The sumbaries us devices bit amine paid is micelianed. This may be equiped by the use of taba
<u> </u>	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
	Numbering	between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
		Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
	Variable Length	Sequence(s) contain n's or Xaa's which represented more than one residue.
		As per the rules, each n or Xaa can only represent a single residue.
		Please present the maximum number of each residue having variable length and
		indicate in the (ix) feature section that some may be missing.
,	PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
	· · · · · · · · · · · · · · · · · · ·	sequence(s) Normally, PatentIn would automatically generate this section from the
		previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
		to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
		sections for Artificial or Unknown sequences.
		אין אין אוווינומו טו טווגווטאוו גבעטבוונבא.
	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
	(OLD RULES)	(2) INFORMATION FOR SEQ ID NO:X:
		(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS"
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
		This sequence is intentionally skipped
		Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
	Skipped Sequences	Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
	(NEW RULES)	<210> sequence id number
	(<400> sequence id number
		000
	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence Listing.
		Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
	(NEW RULES)	
		In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
		a construction of the second
	Use of <213>Organism	Sequence(s) are missing this mandatory field or its response.
	(NEW RULES)	
	Use of <220>Feature	Sequence(s) are missing the <220>Feature and associated headings.
	(NEW RULES)	Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
		Please explain source of genetic material in <220> to <223> section.
		(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Ru
		(SEE FEUERAL REGISTER, 0/01/30, VUL, 03, 140, 104, DD, 23031-321 (SEC, 1.023 01 1164 AG
		(See Federal Register, 0/01/30, Vol. 03, 100, 104, pp. 23031-32) (Sec. 1.823 01 new roo
	Patentin ver 20 "hus"	
	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
	Patentin ver. 2.0 "bug"	

AKS-Biotechnology Systems Branch- 5/15/99

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Does Not Comply

Corrected Diskette Needec

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/636,530 DATE: 08/17/2000 TIME: 10:08:21

Input Set : A:\CIP pharma Sequence Listing Ascii.txt Output Set: N:\CRF3\08162000\1636530.raw

4 <110> APPLICANT: Cantor, Thomas L.

- 6 <120> TITLE OF INVENTION: Parathyroid Hormone Antagonists or Modulators and Uses Theref
- 9 <140> CURRENT APPLICATION NUMBER: US/09/636,530
- 9 <141> CURRENT FILING DATE: 2000-08-10
- WOK 0 <130> FILE REFERENCE:
 - 9 <160> NUMBER OF SEQ ID NOS: 5
 - 11 <170> SOFTWARE: Microsoft Word 2000 ASCII format

ERRORED SEQUENCES

nat Suggestion: Consult new Sequence Rules Globally le fragment 14 <210> SEO ID NO: 1 16 <211> LENGTH: 84 finte 18 <212> TYPE: PRT 20 <213> ORGANISM: human parathyroid hormone peptide fragment 22 <400> SEQUENCE: 1 24 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu 25 1 5 10 27 Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp 28 20 25 30 Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp 31 35 40 45 33 Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val 50 55 34 60 36 Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Jinvalid-do not stow modefication in the Sequence dielf. ide fragment S His Leu Asn 15 su Gln Asp Val 30 10 Arg-lass also 37 65 7.0 E--> 39 Asn Val Leu Thyr Lys Ala Lys Ser Gln 40 80 43 <210> SEQ ID NO: 2 45 <211> LENGTH: 83 [integer length] 47 <212> TYPE: PRT 49 <213> ORGANISM: human parathyroid hormone peptide fragment 51 <400> SEOUENCE: 2 53 Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn 54 1 5 10 56 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Leu Gln Asp Val 57 20 25 60 His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg-Asp Ala 35 40 61 45 63 Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu 64 50 55 60 66 Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn 67 65 70 E--> 69 Val Leu Thyr Lys Ala Lys Ser Gln 70 80 73 <210> SEQ ID NO: 3 75 <211> LENGTH: 51 Fint

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/636,530 DATE: 08/17/2000 TIME: 10:08:21

Input Set : A:\CIP pharma Sequence Listing Ascii.txt
Output Set: N:\CRF3\08162000\I636530.raw

77 <212> TYPE: PRT 79 <213> ORGANISM: human parathyroid hormone peptide fragment 81 <400> SEQUENCE: 3 83 Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser 84 1 -15-E--> 5 10 86 GIn Pro ATY Lys Lys Glu Asp Asn Val Leu Val Glu Ser His 20 25 -30 -> 87 Е-Lys Ser Leu Gly 89 Glu Glu Ala Ash Lys Ala Asp Val Asn Val Leu E--> 90 / 40 45 35 E--> 92/Thyr Tys Ala Lys Ser Gln 50 E--> 93 <210> SEQ ID NO: 4 96 98 <211> LENGTH: 82 *{integer length}* 100 <212> TYPE: PRT 102 <213> ORGANISM: human parathyroid hormone peptide fragment 104 <400> SEQUENCE: 4 106 Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser 107 1 5 10 15 109 Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His 110 20 25 30 112 Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly 113 35 40 45 115 Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser 116 50 55 60 118 His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn Val 119 65 70 75 E--> 121 Leu Thyr Lys Ala Lys Ser Gln 122 80 SEQ ID NO: 5 126 <210> 128 <211> LENGTH: 57 '[integer-longth] 130 <212> TYPE: PRT 132 <213> ORGANISM: human parathyroid hormone peptide fragment 134 <400> SEQUENCE: 5 136 Leu Gln Asp Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala 137 1 5 10 15 139 Pro Arg Asp Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn 140 20 25 30 142 Val Leu Val Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys 40 143 35 45 E--> 145 Ala Asp Val Asn Val Ley Thyr Lys Ala Lys Ser Gln 55 - 1.46, _ _ _ 50

menaligned anivourde -sel ten 4 on Error Junnary Sheet

VERIFICATION SUMMARY D. PATENT APPLICATION: US/09/636,530 T

DATE: 08/17/2000 TIME: 10:08:22

Input Set : A:\CIP pharma Sequence Listing Ascii.txt
Output Set: N:\CRF3\08162000\1636530.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:0 M:201 W: Mandatory field data missing, FILE REFERENCE L:39 M:333 E: Wrong sequence grouping, Amino acids not in groups! . L:69 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:69 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:69 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:84 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 M:332 Repeated in SeqNo=3 L:92 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:92 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:121 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:121 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:145 M:333 E: Wrong sequence grouping, Amino acids not in groups! L:121 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1 L:145 M:333 E: Wrong sequence grouping, Amino acids not in groups!

L:145 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

file://C:\CRF3\Outhold\VsrI636530.htm